

036/0590



# 4

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/022,832

DATE: 04/01/2002

TIME: 16:08:48

Input Set : A:\Biovac15.app

Output Set: N:\CRF3\04012002\J022832.raw

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3 <110> APPLICANT: COUTURE, FRANCE
4     HAMEL, JOSEE
5     BRODEUR, BERNARD R.
6     MARTIN, DENIS
8 <120> TITLE OF INVENTION: NOVEL CHLAMYDIA ANTIGENS AND CORRESPONDING DNA
9     FRAGMENTS
11 <130> FILE REFERENCE: BIOVAC-15
13 <140> CURRENT APPLICATION NUMBER: 10/022,832
14 <141> CURRENT FILING DATE: 2001-12-20
16 <150> PRIOR APPLICATION NUMBER: 60/256,941
17 <151> PRIOR FILING DATE: 2000-12-21
19 <160> NUMBER OF SEQ ID NOS: 77
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 777
25 <212> TYPE: DNA
26 <213> ORGANISM: Chlamydia pneumoniae
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31 aacaaagata ccaatgacat agaattatcc gataatcaaa agttatccag aacatttggt 180
32 catttattag cagcgaatt acgcaagtca gaagatatgt tttttgatat tgcagaagtg 240
33 gctaaggggt tgcaggcgga attgggttgt aaaagtgtc ctttaacaga aacagagtat 300
34 gaagaaaaaa tggctgaagt acagaagttg gtttttgaaa aaaaatcaaa agaaaatctt 360
35 tcattggcag aaaaattctt aaaagaaaat agcaagaacg ctggtgttgt tgaagtgcaa 420
36 ccaagtaaat tgcaatacaa aattattaaa gaaggtgcag ggaaagcaat ttcaggtaaa 480
37 ccttcagctc tattgcacta caagggttcc ttcataatg gccaaagtatt tagcagttca 540
38 gaaggcaaca atgagcctat cttgcttctt ctaggccaaa caattcctgg ttttgcttta 600
39 ggtatgcagg gcatgaaaga aggagaaact cgagttctct acatccatcc tgatcttgct 660
40 tacggaaccg caggacaact tcttccaaac tctttattaa tttttgaaat taacttgatt 720
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45 <211> LENGTH: 258
46 <212> TYPE: PRT
47 <213> ORGANISM: Chlamydia pneumoniae
48 <400> SEQUENCE: 2
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51 1 5 10 15
53 Ser Val Ala Ser Cys Asp Val Arg Ser Lys Asp Lys Asp Lys Asp Gln
54 20 25 30
56 Gly Ser Leu Val Glu Tyr Lys Asp Asn Lys Asp Thr Asn Asp Ile Glu
57 35 40 45
59 Leu Ser Asp Asn Gln Lys Leu Ser Arg Thr Phe Gly His Leu Leu Ala

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62 Arg Gln Leu Arg Lys Ser Glu Asp Met Phe Phe Asp Ile Ala Glu Val
63 65      70      75      80
65 Ala Lys Gly Leu Gln Ala Glu Leu Val Cys Lys Ser Ala Pro Leu Thr
66      85      90      95
68 Glu Thr Glu Tyr Glu Glu Lys Met Ala Glu Val Gln Lys Leu Val Phe
69      100      105      110
71 Glu Lys Lys Ser Lys Glu Asn Leu Ser Leu Ala Glu Lys Phe Leu Lys
72      115      120      125
74 Glu Asn Ser Lys Asn Ala Gly Val Val Glu Val Gln Pro Ser Lys Leu
75      130      135      140
77 Gln Tyr Lys Ile Ile Lys Glu Gly Ala Gly Lys Ala Ile Ser Gly Lys
78 145      150      155      160
80 Pro Ser Ala Leu Leu His Tyr Lys Gly Ser Phe Ile Asn Gly Gln Val
81      165      170      175
83 Phe Ser Ser Ser Glu Gly Asn Asn Glu Pro Ile Leu Leu Pro Leu Gly
84      180      185      190
86 Gln Thr Ile Pro Gly Phe Ala Leu Gly Met Gln Gly Met Lys Glu Gly
87      195      200      205
89 Glu Thr Arg Val Leu Tyr Ile His Pro Asp Leu Ala Tyr Gly Thr Ala
90      210      215      220
92 Gly Gln Leu Pro Pro Asn Ser Leu Leu Ile Phe Glu Ile Asn Leu Ile
93 225      230      235      240
95 Gln Ala Ser Ala Asp Glu Val Ala Ala Val Pro Gln Glu Gly Asn Gln
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98 Gly Glu
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107 <400> SEQUENCE: 3
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110 gtctctttat gtgaagggtgc tgtttagtagaa cttgagaagg tttctaaaga tgaattaata 180
111 aagcaagaag cagatgccta tgttttttgta gagaaatacg gcatatatct aactaagaag 240
112 tgggggatac tcattccttc agcgggggatt gacgagtcca atgttgaagg ttattttgtg 300
113 ttgtatccta gggatttttt gctttccgtg aatactctag gggattgggt aaggaatttc 360
114 tatcatctcg agcattgcgg aatcattata tcggatagtc atacgactcc gttgcgtcgg 420
115 ggaactatgg gtttaggctt atggttgaat ggttttttcc ctttatataa ttatgtagga 480
116 aaaccagatt gttttggtcg tgctttgaag atgacttata gcaatttatt agatggttta 540
117 tcggcagctg cggttctttg tatgggagag ggagacgagc agactcccat tgctattata 600
118 gaggaagctc ccaagattac cttccattct tctccaacta cattacaaga tatgagcact 660
119 ttagcaatcg ctgaggatga agatttatat ggtcctctgc tacaatctat ggcattggaa 720
120 actcccgcaac caacctcctg a 741
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124 <211> LENGTH: 246
125 <212> TYPE: PRT
126 <213> ORGANISM: Chlamydia pneumoniae
128 <400> SEQUENCE: 4

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## RAW SEQUENCE LISTING

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Input Set : A:\Biovac15.app

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130 1 5 10 15
132 Leu Tyr Ser Ile Leu Glu Ser Ser Leu Pro Lys Leu Asn Glu Arg Ser
133 20 25 30
135 Ile Val Val Ile Thr Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val
136 35 40 45
138 Val Glu Leu Glu Lys Val Ser Lys Asp Glu Leu Ile Lys Gln Glu Ala
139 50 55 60
141 Asp Ala Tyr Val Phe Val Glu Lys Tyr Gly Ile Tyr Leu Thr Lys Lys
142 65 70 75 80
144 Trp Gly Ile Leu Ile Pro Ser Ala Gly Ile Asp Glu Ser Asn Val Glu
145 85 90 95
147 Gly Tyr Phe Val Leu Tyr Pro Arg Asp Phe Leu Leu Ser Val Asn Thr
148 100 105 110
150 Leu Gly Asp Trp Leu Arg Asn Phe Tyr His Leu Glu His Cys Gly Ile
151 115 120 125
153 Ile Ile Ser Asp Ser His Thr Thr Pro Leu Arg Arg Gly Thr Met Gly
154 130 135 140
156 Leu Gly Leu Cys Trp Asn Gly Phe Phe Pro Leu Tyr Asn Tyr Val Gly
157 145 150 155 160
159 Lys Pro Asp Cys Phe Gly Arg Ala Leu Lys Met Thr Tyr Ser Asn Leu
160 165 170 175
162 Leu Asp Gly Leu Ser Ala Ala Ala Val Leu Cys Met Gly Glu Gly Asp
163 180 185 190
165 Glu Gln Thr Pro Ile Ala Ile Ile Glu Glu Ala Pro Lys Ile Thr Phe
166 195 200 205
168 His Ser Ser Pro Thr Thr Leu Gln Asp Met Ser Thr Leu Ala Ile Ala
169 210 215 220
171 Glu Asp Glu Asp Leu Tyr Gly Pro Leu Leu Gln Ser Met Ala Trp Glu
172 225 230 235 240
174 Thr Pro Ala Pro Thr Ser
175 245
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180 <212> TYPE: DNA
181 <213> ORGANISM: Chlamydia pneumoniae
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185 ccatcccaat cctctaaagg aatttttgtg gtaaatatga aggaaatgcc acgctccttg 120
186 gatcctggaa aaactcgtct cattgcagac caaactctaa tgcgtcatct atatgaagga 180
187 ctctgcgaag aacattccca aaatggagag attaaaccag cccttcgaga aagctacacc 240
188 atctccgaag acgggactcg gtacacattt aaaatcaaaa acatcctttg gagtaacgga 300
189 gaccctctga cagctcaaga ctttgtctcc tcttggaagg aaatcctaaa ggaagatgcg 360
190 tcctccgtat atctctatgc gtttttacct atcaaaaatg ctcgggcaat ctttgatgat 420
191 actgagtctc cagaaaatct aggagtccga gctttagata agcgtcatct cgaaattcag 480
192 ttagaaactc cctgcgcgca tttcctacat ttcttgactc ttcctatattt tttccctggt 540
193 catgaaactc tgcgaaacta tagcacctct tttgaagaga tgccattac ctgcggtgct 600
194 ttccgcctcg tgtctctaga aaaaggcctg agactccatc tagagaaaaa ccctatgtac 660
195 cataataaaa gccgtgtgaa actacataaa attattgtac agtttatctc aaacgctaac 720

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196 actgcagcca ttctattcaa acataagaaa ttagattggc aaggacctcc ttggggagaa 780
197 cctatccctc cagaaatctc agctttctta catcaagatg accagctctt ttctcttccg 840
198 ggcgcttcga ctacatgggt actctttaat atacaaaaaa aaccttgga caatgctaaa 900
199 ttacgcaagg cattgagcct tgcaatagac aaagatatgt taaccaaagt ggtataccaa 960
200 ggtcttgcaag aacctacaga tcatatccta catccaagac tttatccagg gacctatccc 1020
201 gaacggaaaa gacaaaacga aagaattctt gaggctcaac aactctttga agaagctcta 1080
202 gacgaacttc aaatgacacg cgaagatcta gaaaaggaaa ctttgacttt ctcaaccttt 1140
203 tctttttctt acggaaggat ttgccaaatg ctaagagaac aatggaagaa agtcttaaaa 1200
204 tttactatcc ctatagtagg ccaagagttt ttcacaatac aaaaaaactt cctagagggg 1260
205 aactattccc taaccgtgaa ccaatggacc gcagcattta ttgatccgat gtcttatctc 1320
206 atgatctttg ccaatcctgg aggaatttcc ccctatcacc tccaagattc acactttcaa 1380
207 actctttctc taaagatcac tcaagaacat aaaaaacacc tacgaaatca gcttattatt 1440
208 gaagcccttg actatttaga acactgtcac attctcgaac cactatgtca tccaaatctt 1500
209 cgaattgctt tgaacaaaaa cattaaaaac tttaatcttt ttgttcgacg aacttcagac 1560
210 tttcgtttta tagaaaaact atag 1584

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213 &lt;210&gt; SEQ ID NO: 6

214 &lt;211&gt; LENGTH: 527

215 &lt;212&gt; TYPE: PRT

216 &lt;213&gt; ORGANISM: Chlamydia pneumoniae

218 &lt;400&gt; SEQUENCE: 6

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222 Ser Gly Cys Ser Pro Ser Gln Ser Ser Lys Gly Ile Phe Val Val Asn
223           20           25           30
225 Met Lys Glu Met Pro Arg Ser Leu Asp Pro Gly Lys Thr Arg Leu Ile
226           35           40           45
228 Ala Asp Gln Thr Leu Met Arg His Leu Tyr Glu Gly Leu Val Glu Glu
229           50           55           60
231 His Ser Gln Asn Gly Glu Ile Lys Pro Ala Leu Ala Glu Ser Tyr Thr
232           65           70           75           80
234 Ile Ser Glu Asp Gly Thr Arg Tyr Thr Phe Lys Ile Lys Asn Ile Leu
235           85           90           95
237 Trp Ser Asn Gly Asp Pro Leu Thr Ala Gln Asp Phe Val Ser Ser Trp
238           100          105          110
240 Lys Glu Ile Leu Lys Glu Asp Ala Ser Ser Val Tyr Leu Tyr Ala Phe
241           115          120          125
243 Leu Pro Ile Lys Asn Ala Arg Ala Ile Phe Asp Asp Thr Glu Ser Pro
244           130          135          140
246 Glu Asn Leu Gly Val Arg Ala Leu Asp Lys Arg His Leu Glu Ile Gln
247           145          150          155          160
249 Leu Glu Thr Pro Cys Ala His Phe Leu His Phe Leu Thr Leu Pro Ile
250           165          170          175
252 Phe Phe Pro Val His Glu Thr Leu Arg Asn Tyr Ser Thr Ser Phe Glu
253           180          185          190
255 Glu Met Pro Ile Thr Cys Gly Ala Phe Arg Pro Val Ser Leu Glu Lys
256           195          200          205
258 Gly Leu Arg Leu His Leu Glu Lys Asn Pro Met Tyr His Asn Lys Ser
259           210          215          220
261 Arg Val Lys Leu His Lys Ile Ile Val Gln Phe Ile Ser Asn Ala Asn

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262 225          230          235          240
264 Thr Ala Ala Ile Leu Phe Lys His Lys Lys Leu Asp Trp Gln Gly Pro
265          245          250          255
267 Pro Trp Gly Glu Pro Ile Pro Pro Glu Ile Ser Ala Ser Leu His Gln
268          260          265          270
270 Asp Asp Gln Leu Phe Ser Leu Pro Gly Ala Ser Thr Thr Trp Leu Leu
271          275          280          285
273 Phe Asn Ile Gln Lys Lys Pro Trp Asn Asn Ala Lys Leu Arg Lys Ala
274          290          295          300
276 Leu Ser Leu Ala Ile Asp Lys Asp Met Leu Thr Lys Val Val Tyr Gln
277 305          310          315          320
279 Gly Leu Ala Glu Pro Thr Asp His Ile Leu His Pro Arg Leu Tyr Pro
280          325          330          335
282 Gly Thr Tyr Pro Glu Arg Lys Arg Gln Asn Glu Arg Ile Leu Glu Ala
283          340          345          350
285 Gln Gln Leu Phe Glu Glu Ala Leu Asp Glu Leu Gln Met Thr Arg Glu
286          355          360          365
288 Asp Leu Glu Lys Glu Thr Leu Thr Phe Ser Thr Phe Ser Phe Ser Tyr
289          370          375          380
291 Gly Arg Ile Cys Gln Met Leu Arg Glu Gln Trp Lys Lys Val Leu Lys
292 385          390          395          400
294 Phe Thr Ile Pro Ile Val Gly Gln Glu Phe Phe Thr Ile Gln Lys Asn
295          405          410          415
297 Phe Leu Glu Gly Asn Tyr Ser Leu Thr Val Asn Gln Trp Thr Ala Ala
298          420          425          430
300 Phe Ile Asp Pro Met Ser Tyr Leu Met Ile Phe Ala Asn Pro Gly Gly
301          435          440          445
303 Ile Ser Pro Tyr His Leu Gln Asp Ser His Phe Gln Thr Leu Leu Ile
304          450          455          460
306 Lys Ile Thr Gln Glu His Lys Lys His Leu Arg Asn Gln Leu Ile Ile
307 465          470          475          480
309 Glu Ala Leu Asp Tyr Leu Glu His Cys His Ile Leu Glu Pro Leu Cys
310          485          490          495
312 His Pro Asn Leu Arg Ile Ala Leu Asn Lys Asn Ile Lys Asn Phe Asn
313          500          505          510
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327 gctaagtaca tactatttgc aattgcagcc acatcaggag cactcggaac aattctaggt 180
328 ctatctggag cgctaacccc aggaataggt attgcccttc ttgttatctt cttgttttct 240
329 atggtgcttt taggtttaat ccttaaagat tctataagtg gaggagaaga acgcaggctc 300
330 agagaagagg tctctcgatt tacaagtgag aatcaacggt tgacagtcac aaccacaaca 360
331 cttgagactg aagtaaagga tttaaaagca gctaaagatc aacttacact tgaaatcgaa 420

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VERIFICATION SUMMARY

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